

PCT 09.

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/137,559

CRF Processing Date: \_\_\_\_\_  
Edited by: \_\_\_\_\_  
Verified by: \_\_\_\_\_ (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning end of files; ☐ secretary initials/filename at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

PCT  
09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/787,559

DATE: 04/04/2001

TIME: 11:26:47

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04042001\I787559.raw

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3 <110> APPLICANT: Kramer, Michael
5 <120> TITLE OF INVENTION: Regulatory Protein from Keratinocytes
7 <130> FILE REFERENCE: KML/PCT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/787,559
C--> 10 <141> CURRENT FILING DATE: 2001-03-19
12 <150> PRIOR APPLICATION NUMBER: DE19842863.4
13 <151> PRIOR FILING DATE: 1998-09-19
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2533
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <400> SEQUENCE: 1
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26 gccagagtca gggccagcag aagccctcc ggggtgggtt ttacgacatc gaggcgacc 120
27 tgggcaaaag caacttcgcg gtggtgaagc tggcgcggca tcgagtcacc aaaacgcag 180
28 ttgcaataaa aataattgat aaaacacgat tagattcaag caatttgag aaaatctatc 240
29 gtgaggttca gctgatgaag cttctgaacc atccacacat cataaagctt taccagggtta 300
30 tggaaacaaa ggacatgctt tacatcgtca ctgaatttgc taaaaatgga gaaatgtttg 360
31 attatttgac ttccaacygg cactcgagtg agaacyaggc gcggaagaag ttctggcaaa 420
32 tcctgtcggc cgtggagtac tgtcacgacc atcacatcgt ccaccgggac ctcaagaccg 480
33 agaacctcct gctggatggc aacatggaca tcaagctggc agattttgga tttgggaatt 540
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36 tgetgtacgt cctggtctgc ggttctctcc ccttcgatgg gcctaacctg ccgacgctga 720
37 gacagcggtt gctggagggc cgttccgca tccctctctt catgtctcaa gactgtgaga 780
38 gcctgatccg ccgcatgctg gtggtggacc ccgccaggcg catcaccatc gccagatcc 840
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44 aggtgcctca ggaaggtctt tccaccgacc ctttccgacc tgccttgctg tgcgcgagc 1200
45 cgcagacctt ggtgcagtc gtctccagg ccgagatgga ctgtgagctc cagagctcgc 1260
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55 ccacgcggac caaagggttt ctgggactga acaaaatcaa ggggctggt cggcagggtg 1860
56 gccaggctcc tgcagccgg gccagcagg gcggcctgag ccccttccac gccctgcac 1920
57 agagcccgag cctgcacggc gggcagcgg gcagccggga gggctggagc ctgctggagg 1980

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DATE: 04/04/2001

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58 aggtgctaga gcagcagagg ctgctccagt tacagcacca cccggccgct gcacccggct 2040
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60 gggctgcccc gctccccagc accctctca cgtcggggct cccgctgctg ccgccccac 2160
61 tctgcagac .cggcgcgtcc cccgtggcct cagcggcgca gctcctggac acacacctgc 2220
62 acattggcac cggccccacc gccctccccg ctgtgcccc accacgcctg gccaggctgg 2280
63 cccaggttg tgagccccctg gggctgctgc agggggactg tgagatggag gacctgatgc 2340
64 cctgctccct aggcacgttt gtctggtgc agtgagggca gccctgcac ctggcacgga 2400
65 cactgactct tacagcaata acttcagagg aggtgaagac atctggcctc aaagccaaga 2460
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71 &lt;210&gt; SEQ ID NO: 2

72 &lt;211&gt; LENGTH: 790

73 &lt;212&gt; TYPE: PRT

74 &lt;213&gt; ORGANISM: Homo sapiens

76 &lt;220&gt; FEATURE:

77 &lt;223&gt; OTHER INFORMATION: Serine/Threonine kinase motif

79 &lt;220&gt; FEATURE:

80 &lt;223&gt; OTHER INFORMATION: 4 Tyrosine kinase phosphorylation sites

82 &lt;220&gt; FEATURE:

83 &lt;223&gt; OTHER INFORMATION: Kinase domain with ATP-binding site

85 &lt;400&gt; SEQUENCE: 2

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86 His Pro Gly Ala Arg Gly Ala Met Val Ile Met Ser Glu Phe Ser Ala
87 1 5 10 15
89 Asp Pro Ala Gly Gln Ser Gln Gly Gln Lys Pro Leu Arg Val Gly
90 20 25 30
92 Phe Tyr Asp Ile Glu Arg Thr Leu Gly Lys Gly Asn Phe Ala Val Val
93 35 40 45
95 Lys Leu Ala Arg His Arg Val Thr Lys Thr Gln Val Ala Ile Lys Ile
96 50 55 60
98 Ile Asp Lys Thr Arg Leu Asp Ser Ser Asn Leu Glu Lys Ile Tyr Arg
99 65 70 75 80
101 Glu Val Gln Leu Met Lys Leu Leu Asn His Pro His Ile Ile Lys Leu
102 85 90 95
104 Tyr Gln Val Met Glu Thr Lys Asp Met Leu Tyr Ile Val Thr Glu Phe
105 100 105 110
107 Ala Lys Asn Gly Glu Met Phe Asp Tyr Leu Thr Ser Asn Gly His Leu
108 115 120 125
110 Ser Glu Asn Glu Ala Arg Lys Lys Phe Trp Gln Ile Leu Ser Ala Val
111 130 135 140
113 Glu Tyr Cys His Asp His His Ile Val His Arg Asp Leu Lys Thr Glu
114 145 150 155 160
116 Asn Leu Leu Leu Asp Gly Asn Met Asp Ile Lys Leu Ala Asp Phe Gly
117 165 170 175
119 Phe Gly Asn Phe Tyr Lys Ser Gly Glu Pro Leu Ser Thr Trp Cys Gly
120 180 185 190
122 Ser Pro Pro Tyr Ala Ala Pro Glu Val Phe Glu Gly Lys Glu Tyr Glu
123 195 200 205
125 Gly Pro Gln Leu Asp Ile Trp Ser Leu Gly Val Val Leu Tyr Val Leu
126 210 215 220

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129 225 230 235 240
131 Gln Arg Val Leu Glu Gly Arg Phe Arg Ile Pro Phe Phe Met Ser Gln
132 245 250 255
134 Asp Cys Glu Ser Leu Ile Arg Arg Met Leu Val Val Asp Pro Ala Arg
135 260 265 270
137 Arg Ile Thr Ile Ala Gln Ile Arg Gln His Arg Trp Met Arg Ala Glu
138 275 280 285
142 Pro Cys Leu Pro Gly Pro Ala Cys Pro Ala Phe Ser Ala His Ser Tyr
143 290 295 300
145 Thr Ser Asn Leu Gly Asp Tyr Asp Glu Gln Ala Leu Gly Ile Met Gln
146 305 310 315 320
148 Thr Leu Gly Val Asp Arg Gln Arg Thr Val Glu Ser Leu Gln Asn Ser
149 325 330 335
151 Ser Tyr Asn His Phe Ala Ala Ile Tyr Tyr Leu Leu Leu Glu Arg Leu
152 340 345 350
154 Lys Glu Tyr Arg Asn Ala Gln Cys Ala Arg Pro Gly Pro Ala Arg Gln
155 355 360 365
157 Pro Arg Pro Arg Ser Ser Asp Leu Ser Gly Leu Glu Val Pro Gln Glu
158 370 375 380
160 Gly Leu Ser Thr Asp Pro Phe Arg Pro Ala Leu Leu Cys Pro Gln Pro
161 385 390 395 400
163 Gln Thr Leu Val Gln Ser Val Leu Gln Ala Glu Met Asp Cys Glu Leu
164 405 410 415
166 Gln Ser Ser Leu Gln Trp Pro Leu Phe Phe Pro Val Asp Ala Ser Cys
167 420 425 430
169 Ser Gly Val Phe Arg Pro Arg Pro Val Ser Pro Ser Ser Leu Leu Asp
170 435 440 445
172 Thr Ala Ile Ser Glu Glu Ala Arg Gln Gly Pro Gly Leu Glu Glu Glu
173 450 455 460
175 Gln Asp Thr Gln Glu Ser Leu Pro Ser Ser Thr Gly Arg Arg His Thr
176 465 470 475 480
178 Leu Ala Glu Val Ser Thr Arg Leu Ser Pro Leu Thr Ala Pro Cys Ile
179 485 490 495
181 Val Val Ser Pro Ser Thr Thr Ala Ser Pro Ala Glu Gly Thr Ser Ser
182 500 505 510
184 Asp Ser Cys Leu Thr Phe Ser Ala Ser Lys Ser Pro Ala Gly Leu Ser
185 515 520 525
187 Gly Thr Pro Ala Thr Gln Gly Leu Leu Gly Ala Cys Ser Pro Val Arg
188 530 535 540
190 Leu Ala Ser Pro Phe Leu Gly Ser Gln Ser Ala Thr Pro Val Leu Gln
191 545 550 555 560
193 Ala Gln Gly Gly Leu Gly Gly Ala Val Leu Leu Pro Val Ser Phe Gln
194 565 570 575
196 Glu Gly Arg Arg Ala Ser Asp Thr Ser Leu Thr Gln Gly Leu Lys Ala
197 580 585 590
199 Phe Arg Gln Gln Leu Arg Lys Thr Thr Arg Thr Lys Gly Phe Leu Gly
200 595 600 605
202 Leu Asn Lys Ile Lys Gly Leu Ala Arg Gln Val Cys Gln Val Pro Ala

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205 Ser Arg Ala Ser Arg Gly Gly Leu Ser Pro Phe His Ala Pro Ala Gln
206 625      630      635      640
208 Ser Pro Gly Leu His Gly Gly Ala Ala Gly Ser Arg Glu Gly Trp Ser
209      645      650      655
213 Leu Leu Glu Glu Val Leu Glu Gln Gln Arg Leu Leu Gln Leu Gln His
214      660      665      670
216 His Pro Ala Ala Ala Pro Gly Cys Ser Gln Ala Pro Gln Pro Ala Pro
217      675      680      685
219 Ala Pro Phe Val Ile Ala Pro Cys Asp Gly Pro Gly Ala Ala Pro Leu
220      690      695      700
222 Pro Ser Thr Leu Leu Thr Ser Gly Leu Pro Leu Leu Pro Pro Pro Leu
223 705      710      715      720
225 Leu Gln Thr Gly Ala Ser Pro Val Ala Ser Ala Ala Gln Leu Leu Asp
226      725      730      735
228 Thr His Leu His Ile Gly Thr Gly Pro Thr Ala Leu Pro Ala Val Pro
229      740      745      750
231 Pro Pro Arg Leu Ala Arg Leu Ala Pro Gly Cys Glu Pro Leu Gly Leu
232      755      760      765
234 Leu Gln Gly Asp Cys Glu Met Glu Asp Leu Met Pro Cys Ser Leu Gly
235      770      775      780
237 Thr Phe Val Leu Val Gln
238 785      790
243 <210> SEQ ID NO: 3
244 <211> LENGTH: 823
245 <212> TYPE: PRT
246 <213> ORGANISM: Homo sapiens
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Serine/Threonine kinase motif
251 <220> FEATURE:
252 <223> OTHER INFORMATION: 4 Tyrosine kinase phosphorylation sites
254 <220> FEATURE:
255 <223> OTHER INFORMATION: kKinase domaine with ATP binding site
257 <400> SEQUENCE: 3
258 Pro Glu Ala Ala Ala Ala Ala Ala Gly Ala Val Gly Thr Arg
259 1      5      10      15
261 Ala Ala Pro Ala Ala Glu Arg Ala Ala Ser Trp Pro Gly Arg Ser Gly
262      20      25      30
264 Gly Gly Gly Gly Ala Arg Gly Ala Met Val Ile Met Ser Glu Phe Ser
265      35      40      45
267 Ala Asp Pro Ala Gly Gln Ser Gln Gly Gln Gln Lys Ser Leu Arg Val
268      50      55      60
270 Gly Phe Tyr Asp Ile Glu Arg Thr Leu Gly Lys Gly Asn Phe Ala Val
271 65      70      75      80
273 Val Lys Leu Ala Arg His Arg Val Thr Lys Thr Gln Val Ala Ile Lys
274      85      90      95
276 Ile Ile Asp Lys Thr Arg Leu Asp Ser Ser Asn Leu Glu Lys Ile Tyr
277      100      105      110
279 Arg Glu Val Gln Leu Met Lys Leu Leu Asn His Pro His Ile Ile Lys

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280	115	120	125
282 Leu Tyr Gln Val Met Glu Thr Lys Asp Met Leu Tyr Ile Val Thr Glu			
283 130	135	140	
285 Phe Ala Lys Asn Gly Glu Met Phe Asp Tyr Leu Thr Ser Asn Gly His			
286 145	150	155	160
288 Leu Ser Glu Asn Glu Ala Arg Lys Lys Phe Trp Gln Ile Leu Ser Ala			
289 165	170	175	
291 Val Glu Tyr Cys His Asp His His Ile Val His Arg Asp Leu Lys Thr			
292 180	185	190	
294 Glu Asn Leu Leu Leu Asp Gly Asn Met Asp Ile Lys Leu Ala Asp Phe			
295 195	200	205	
297 Gly Phe Gly Asn Phe Tyr Lys Ser Gly Glu Pro Leu Ser Thr Trp Cys			
298 210	215	220	
300 Gly Ser Pro Pro Tyr Ala Ala Pro Glu Val Phe Glu Gly Lys Glu Tyr			
301 225	230	235	240
303 Glu Gly Pro Gln Leu Asp Ile Trp Ser Leu Gly Val Val Leu Tyr Val			
304 245	250	255	
306 Leu Val Cys Gly Ser Leu Pro Phe Asp Gly Pro Asn Leu Pro Thr Leu			
307 260	265	270	
309 Arg Gln Arg Val Leu Glu Gly Arg Phe Arg Ile Pro Phe Phe Met Ser			
310 275	280	285	
314 Gln Asp Cys Glu Ser Leu Ile Arg Arg Met Leu Val Val Asp Pro Ala			
315 290	295	300	
317 Arg Arg Ile Thr Ile Ala Gln Ile Arg Gln His Arg Trp Met Arg Ala			
318 305	310	315	320
320 Glu Pro Cys Leu Pro Gly Pro Ala Cys Pro Ala Phe Ser Ala His Ser			
321 325	330	335	
323 Tyr Thr Ser Asn Leu Gly Asp Tyr Asp Glu Gln Ala Leu Gly Ile Met			
324 340	345	350	
326 Gln Thr Leu Gly Val Asp Arg Gln Arg Thr Val Glu Ser Leu Gln Asn			
327 355	360	365	
329 Ser Ser Tyr Asn His Phe Ala Ala Ile Tyr Tyr Leu Leu Leu Glu Arg			
330 370	375	380	
332 Leu Lys Glu Tyr Arg Asn Ala Gln Cys Ala Arg Pro Gly Pro Ala Arg			
333 385	390	395	400
335 Gln Pro Arg Pro Arg Ser Ser Asp Leu Ser Gly Leu Glu Val Pro Gln			
336 405	410	415	
338 Glu Gly Leu Ser Thr Asp Pro Phe Arg Pro Ala Leu Leu Cys Pro Gln			
339 420	425	430	
341 Pro Gln Thr Leu Val Gln Ser Val Leu Gln Ala Glu Met Asp Cys Glu			
342 435	440	445	
344 Leu Gln Ser Ser Leu Gln Trp Pro Leu Phe Phe Pro Val Asp Ala Ser			
345 450	455	460	
347 Cys Ser Gly Val Phe Arg Pro Arg Pro Val Ser Pro Ser Ser Leu Leu			
348 465	470	475	480
350 Asp Thr Ala Ile Ser Glu Glu Ala Arg Gln Gly Pro Gly Leu Glu Glu			
351 485	490	495	
353 Glu Gln Asp Thr Gln Glu Ser Leu Pro Ser Ser Thr Gly Arg Arg His			
354 500	505	510	

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/787,559

DATE: 04/04/2001

TIME: 11:26:48

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04042001\I787559.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date